

TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase
JOURNAL Science 284 (5414), 657-661 (1999)
MEDLINE 99234320
PUBMED 10213691
REFERENCE 2 (bases 1 to 508)
AUTHORS Kanura, T., Lane, W.S., Conaway, R.C. and Conaway, J.W.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA

FEATURES
SOURCE
1. 508
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. 508
/gene="RBX1"
7. 333
/gene="RBX1"
/note="Ring finger-like protein; component of VHL tumor suppressor complex and SCF ubiquitin ligase"
/product="ring-box protein 1"
/codon_start=1
/product="ring-box protein 1"
/protein_id="AAD29715.1"
/db_xref="GI:4769004"
/translation="MAAMDVDPGSGNSAGKKRFEVKKMNAVALMAMDIVDNCAI
CRNHIMDLICQANQASATSECTVAMGVGNHAFHCHISRLKTRQVPLDNRME
FQKXGH"

BASE COUNT 126 a 106 c 124 g 152 t
ORIGIN

Query Match 100.0% Score 508, DB 9, Length 508;
Best Local Similarity 100.0%; Pred. No. 6, 1e-126;
Matches 508: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 CCCAAATGGCGGCGAGCATGTGATACCCGAGCGGACCAAGCGCGCGGC 60
Db 1 CCCAAATGGCGGCGAGCATGTGATACCCGAGCGGACCAAGCGCGGC 60
OY 61 AAGAAGCGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 120
Db 61 AAGAAGCGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 120
OY 121 GTGATTAAGTGGCATGTGAGGAAACCAATATGATCTTTGATAGATGTCA 180
Db 121 GTGATTAAGTGGCATGTGAGGAAACCAATATGATCTTTGATAGATGTCA 180
OY 181 AACGAGCGGCGGCTACTTCAAGAGAGTACTGTGCGATGGGAGTCTGA 240
Db 181 AACGAGCGGCGGCTACTTCAAGAGAGTACTGTGCGATGGGAGTCTGA 240
OY 241 TTTCACCTTCACATCTCTCGCTGCTCAAAACAGAGGTGTCTCATTTG 300
Db 241 TTTCACCTTCACATCTCTCGCTGCTCAAAACAGAGGTGTCTCATTTG 300
OY 301 AGAGAGTGGGAATTCACAAAGTATGAGGACATAGAGAAAGACTCTTC 360
Db 301 AGAGAGTGGGAATTCACAAAGTATGAGGACATAGAGAAAGACTCTTC 360
OY 361 TGTGTTGTTATTCATTTAATGACTTTCCTGCTGTACTCAATATACAA 420
Db 361 TGTGTTGTTATTCATTTAATGACTTTCCTGCTGTACTCAATATACAA 420
OY 421 CTGCTGTTTCTGCTTGTGTTTCTGAGTTGCTGTTCTGTAAGCAAT 480
Db 421 CTGCTGTTTCTGCTTGTGTTTCTGAGTTGCTGTTCTGTAAGCAAT 480
OY 481 TGTCAAAATTAAGTCCAGTTGATCTGG 508
Db 481 TGTCAAAATTAAGTCCAGTTGATCTGG 508

```

RESULT 2
BC001466

LOCUS BC001466 544 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, ring-box 1, clone MGC:1481 IMAGE:3138751, mRNA,
complete cds.
ACCESSION BC001466
VERSION BC001466.1 GI:12655214
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 544)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantipop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L. H. and Green, E.D.

FEATURES
source
1. 544
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="locus:3138751"
/clone="MGC:1481 IMAGE:3138751"
/tissue="MGC:Placenta, choriocarcinoma"
/clone_1db="NIH-MGC-21"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
15. 341
/codon_start=1
/product="ring-box 1"
/protein_id="AAH01466.1"
/db_xref="GI:12655215"
/translation="MAAMDVDPGSGNSAGKKRFEVKKMNAVALMAMDIVDNCAI
CRNHIMDLICQANQASATSECTVAMGVGNHAFHCHISRLKTRQVPLDNRME
FQKXGH"

BASE COUNT 157 a 107 c 129 g 151 t
ORIGIN

Query Match 97.4% Score 495, DB 9, Length 544;
Best Local Similarity 99.8%; Pred. No. 1, 9e-122;
Matches 506: Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

OY 2 CCAAAATGGCGGCGAGCATGTGATACCCGAGCGGACCAACAGCGCGGCA 61
Db 10 CCAAAATGGCGGCGAGCATGTGATACCCGAGCGGACCAACAGCGCGGCA 69
OY 62 AGAAGCGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 121
Db 70 AGAAGCGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 129
OY 122 TTGATTAAGTGGCATGTGAGGAAACCAATTAATGATCTTTGATAGAT 181

```

CDS	ORIGIN	BASE COUNT
<pre> /note="Vector: pDNR-Lib" 23..349 /codon_start=1 /product="ring-box 1" /protein_id="AAH7370.1" /db_xref="GI:15924202" /translation="MAAAMDVDPPTGNSGAKRREYVKKNVAVALWAMDIVYDNCAI CRHHMDLCECOANQASATSECTVAMVGCNHAHFHCISRWLKTROYCVPLDNRWE FOKKYH" </pre>	<pre> 157 a 107 c 133 g 157 t </pre>	<pre> Query Match 97.1%; Score 493.4; DB 9; Length 554; Best Local Similarity 99.6%; Pred. No. 5.2e-122; Matches 505; Conservative 0; Mismatches 1; Indels 1; Caps 1; </pre>
<pre> 2 CCAAAATGGCGGCGAGCGATGATGTACCCGAGCGGCGACCAACAGCGGGCGGGGCA 61 18 CCAAAATGGCGGCGAGCGATGATGTACCCGAGCGGCGACCAACAGCGGGCGGGCA 77 </pre>		
<pre> 62 AGAAGCGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCGCTGGGATATTGTGG 121 78 AGAAGCGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCGCTGGGATATTGTGG 137 </pre>		
<pre> 122 TTGATTAAGTGCATCTGCAGGAACCAATTATGATCTTTGCATTAGATAGTCAAGCTA 181 </pre>		

QY	182	ACCAGGCGTCGGACTTTCACAAAGAGTGTACTGTGTGCATGGGAGTCTGTAAACCATGCTT	241
Db	198	ACCAAGGCGTCGGCTTACTTCAGAAAGAGTGTACTGTGTGCATGGGAGTCTGTAAACCATGCTT <td>257</td>	257
QY	242	TTCACTTCCACTGCATCTCTGTGCTCAAAACACGACAGGTGTGTCCATTGGACAACA	301
Db	258	TTCACTTCCACTGCATCTCTGTGCTCAAAACACGACAGGTGTGTCCATTGGACAACA	317
QY	302	GAGAGTGGGAATTTCCAAAGATATGGGCATGAGAAAACATCTTCCATTCAAAGCTTAAT	361
Db	318	GAGAGTGGGAATTTCCAAAGATATGGGCATGAGAAAACATCTTCCATTCAAAGCTTAAT	377
QY	362	GTTTGTATTATCATTTAATTAATGACTTTCCCTGCTGTACTTAATTAACAATATGGATGAGAC	421
Db	378	GTTTGTATTATCATTTAATTAATGACTTTCCCTGCTGTACTTAATTAACAATATGGATGAGAC	436
QY	422	TGTGTTTTTCTGCTTGTGTTTTTTCAGTTGCTGTCTGTAGCCATATTGTATTTCTGT	481
Db	437	TGTGTTTTTCTGCTTGTGTTTTTTCAGTTGCTGTCTGTAGCCATATTGTATTTCTGT	496
QY	482	GTCAAATTAAGTCCAGTTGATTCGG	508
Db	497	GTCAAATTAAGTCCAGTTGATTCGG	523
RESULT 4			
HUMY060A05			
LOCUS	HUMY060A05	497 bp	mRNA linear
DEFINITION	Homo sapiens full length insert cDNA clone y060A05.		PRI 29-AUG-1998
ACCESSION	AF085906		
VERSION	AF085906.1		GI:3483246
KEYWORDS	FLI cDNA.		
SOURCE	Homo sapiens.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 497)	Woeßner, J., Tan, F., Marra, M., Kucaba, T., Vandell, M., Martin, J., Math, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Theising, B., Getseil, S., Allen, M., Underwood, K., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurr, R., Ritter, E., Koh, S., Shaller, T., Belymer, K., Hillier, L., Wilson, R., and Waterston, R.	Full Clone Sequencing of the Longest Available Member from Each Unigene Cluster

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 497)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
SUBMITTED BY: Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@wustl.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

SIMILARITY INFORMATION:
Similar to Caenorhabditis elegans protein Z70757 (PID:g1262999)
ZK287.5

The location of this clone is unknown.

FEATURES
source Location/Qualifiers

1..497
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:200144"
/clone_lib="Sources:fetal_liver_spleen_1NPLS"
3..305
/note="Similar to Caenorhabditis elegans protein Z70757 (PID:g1262999)"
18..284
/note="Similar to Caenorhabditis elegans protein U80449 (PID:g1707068)"
36..302
/note="Similar to Saccharomyces cerevisiae protein S66830 (PID:g2132017)"
42..302
/note="Similar to Schizosaccharomyces pombe protein Z98977 (PID:g2388937)"
51..284
/note="Similar to Caenorhabditis elegans protein Z46242 (PID:g559430)"
misc_feature
misc_feature
misc_feature
misc_feature
BASE COUNT 131 a 101 c 117 g 148 t
ORIGIN

Query Match 92.7%; Score 471; DB 9; Length 497;
Best Local Similarity 99.8%; Pred. No. 5.5e-116;
Matches 482; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

26 TGGATACCCGAGGCGCAACAGCGGCGGAGAGAGCGTTGATGAGTGAAGAAAGT 85
|||||
Db 1 TGGATACCCGAGGCGCAACAGCGGCGGAGAGAGCGTTGATGAGTGAAGAAAGT 60
GGAATGACGAGCCCTGCGGCTGGGATATTGGTGTGATTAAGTGCATCTTCACAGA 145
|||||
Db 61 GGAATGACGAGCCCTGCGGCTGGGATATTGGTGTGATTAAGTGCATCTTCACAGA 120
GACATCTGCGTGGCTCAAAACAGACAGTGTGTCCATTGGAGAGTGGGAAAT 3004
|||||
Db 314 TCCTCAAAATATGAGGAGCCTAGAGAAAGACTTCTTCATCAATCAATTTGTTTATTC 373
|||||
Db 3005 TCCTCAAAATATGAGGAGCCTAGAGAAAGACTTCTTCATCAATCAATTTGTTTATTC 3064
|||||
QY 206 AGTACTGTCGATGGGAGAGTGTACCAATGCTTTCACATGCAAGCAATCTCGCT 265
|||||

Db 181 AGTACTGTCGATGGGAGAGTGTACCAATGCTTTCACATGCAATCTCGCT 240
QY 266 GGCCTCAAAACAGACAGAGTGTGTCCATTGGACACAGAGAGTGGAAATTC:AAAGATG 325
|||||
Db 241 GGCCTCAAAACAGACAGAGTGTGTCCATTGGACACAGAGAGTGGAAATTC:AAAGATG 300
GACACTAGAGAAAGACTTTCATCAAGCTTAATTTGTTTATTCATTTAATTACT 385
|||||
Db 301 GGCCTAGAGAAAGACTTTCATCAAGCTTAATTTGTTTATTCATTTAATTACT 359
QY 386 TTCCCTGCTGTACTTATTAATCAATGAGAGAGTGTGTTCCTGCTTTT 445
Db 360 TTCCCTGCTGTACTTATTAATCAATGAGAGAGTGTGTTCCTGCTTTT 419
QY 446 TCAGTTGCTGTTCTGTAGCCATATTGTATTCGTGTCAATTAAGTCCAGTTGATTC 505
Db 420 TCAGTTGCTGTTCTGTAGCCATATTGTATTCGTGTCAATTAAGTCCAGTTGATTC 479
QY 506 TGG 508
|||
Db 480 TGG 482

RESULT 5
AX212267
LOCUS AX212267 3208 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 27 from Patent WO0159134.
ACCESSION AX212267
VERSION AX212267.1 GI:15524031
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3208)
Donoho, G., Scoville, J., Turner, C.A., Friedrich, G.B., Abuin, A.,
Zambrowicz, B. and Sands, A.T.
Human proteases and polynucleotides encoding the same
Patent: WO 0159134-A 27 16-AUG-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
1..3208
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 882 a 750 c 772 g 804 t
ORIGIN
Query Match 81.7%; Score 415; DB 6; Length 3208;
Best Local Similarity 98.6%; Pred. No. 6.9e-101;
Matches 429; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 74 AAGTGAAAAGTGAATGACATGACCCCTGCGGCTGGGATATTGTGATTAAGTGTG 133
|||||
Db 2765 AAAAAAATGATGATGACATGACCCCTGCGGCTGGGATATTGTGATTAAGTGTG 2824
CCATCTGAGAGACACATTTATGATCTTTCATAGAAATGTCAAGCTAACAGCGTCCG 193
|||||
Db 2825 CCATCTGAGAGACACATTTATGATCTTTCATAGAAATGTCAAGCTAACAGCGTCCG 2884
CTACTTCGAGAGAGTGTCTGCGATGGGAGAGTGTGAACATGCTTTCATCTCACT 253
|||||
QY 194 CTACTTCGAGAGAGTGTCTGCGATGGGAGAGTGTGAACATGCTTTCATCTCACT 253
Db 2885 CTACTTCGAGAGAGTGTCTGCGATGGGAGAGTGTGAACATGCTTTCATCTCACT 2944
GCATCTGCGTGGCTCAAAACAGACAGTGTGTCCATTGGAGACAGAGTGGGAAAT 313
|||||
QY 254 GCATCTGCGTGGCTCAAAACAGACAGTGTGTCCATTGGAGACAGAGTGGGAAAT 313
Db 2945 GCATCTGCGTGGCTCAAAACAGACAGTGTGTCCATTGGAGACAGAGTGGGAAAT 3004
TCCTCAAAATATGAGGAGCCTAGAGAAAGACTTCTTCATCAATCAATTTGTTTATTC 373
|||||
Db 3005 TCCTCAAAATATGAGGAGCCTAGAGAAAGACTTCTTCATCAATCAATTTGTTTATTC 3064
|||||
QY 374 ATTAATGATTTCCGCTGTTACCAATTAATTAAGTGAAGTGTGTTTTC 433
|||||

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: CAGAAATCCAACCTGGACTTTATTTG
Primer B: TTATTCATTTAATGACTTTCCTGCC
SFS size: 139
PCR profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation:	94 degrees C for 15 seconds
Annealing:	62 degrees C for 23 seconds
Polymerization:	72 degrees C for 30 seconds
PCR Cycles:	30
Thermal Cycler:	Perkin Elmer 9600
Protocol:	
Template:	25 ng
Primer:	each 1 uM
dNTPs:	each 200 uM
Taq Polymerase:	0.05 units/uL
Total Vol:	10 uL

Buffer:	
MgCl ₂ :	2.5 mM
KCl:	50 mM
Tris-HCl:	20 mM
pH:	8.3

Prepared with primer pairs provided by Sandoz, derived from D52875
 -- Washington University/Merck EST sequence.
 Location/Qualifiers

FEATURES	location/Qualifiers
source	1..433
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/map="10"
STS	1..139
primer_bind	1..24
primer_bind	complement(115..139)
BASE COUNT	139 a 100 c 87 g 107 t
ORIGIN	

Query Match	77.2%;	Score 392;	DB 11;	Length 433;
Best Local Similarity	98.2%;	Pred. No. 9.9e-95;		

Matches 428; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

QY	72	TGAAGTAAATAATGAAATGCAAGTACCCCTCGGGGCGTGGGATATATGTGGTATAC	13
Db	433	TGAAGTAAATAATGAAATGCAAGTACCC -CTGGGCGTGGGATATATGTGGTATAC	37
QY	132	TGGCATTCTGCAGGAACCACTATTATGATCTTTTGGATGAATGTCAAGCTAACCGAGCGTC	19
Db	374	TGGCATTCTGCAGGAACCACTATTATGATGAGTATGATGAATGTCAAGCTAACCGAGCGTC	31
QY	192	CGCTACTTCAGGAAGATGTACTGTGGCATGGGGAGTCTGTACCACTGCTTTTCACTTCCA	25
Db	314	CGCTACTTCAGGAAGATGTACTGTGGCATGGGGAGTCTGTACCACTGCTTTTCACTTCCA	25
QY	252	CTGCATCTCTCGCTGTGCTTAAACACGACAGAGTGTGTCCATTGGACACAGAGAGTGGGA	31
Db	255	CTGCATCTCTCGCTGTGCTTAAACACGACAGAGTGTGTCCATTGGACACAGAGAGTGGGA	19
QY	312	ATTCCAAAAGATAGGCGACATAGAAAAGACTTCTTCATCAAGCTTAATTTGTGTAT	37
Db	195	ATTCCAAAAGATAGGCGACATAGAAAAGACTTCTTCATCAAGCTTAATTTGTGTAT	13
QY	372	TCAATTAATTAAGATTCCTCGCTGTACTTAATTAACAAATGGATGGAACTGTGTTT	43
Db	135	TCAATTAATTAAGATTCCTCGCTGTACTTAATTAACAAATGGATGGAACTGTGTTT	77
QY	432	TCTGCTTTGTTTTTCAGTTTCTTTCATAGCCATATTTGATTTCTGTCAATAA	49
Db	76	TCTGCTTTGTTTTTCAGTTTCTTTCATAGCCATATTTGATTTCTGTGTCAATAA	17
QY	492	GTCACAGTTGGATTCG 507	
Db	16	GTCACAGTTGGATTCG 1	

RESULT 7	LOCUS	DEFINITION
AC109638	104787 bp	DNA linear PRI 09-MAR-2002
AC109638		Homo sapiens BAC clone RP11-495B16 from 2, complete sequence.

ACCESSION	AC109638	AC069095
VERSION	AC109638.2	GI:18767595
KEYWORDS	HTG.	
SOURCE	Homo sapiens.	

ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 104787)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence.
Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074

REFERENCE

AUTHORS Waligorski, J. and Cotton, M.
TITLE The sequence of Homo sapiens BAC clone RP11-495B16
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 104787)

AUTHORS

REFERENCE
4 (bases 1 to 104787)
MO 63108, USA
University School of Medicine, 444 Forest Park Parkway, St. Louis,
Submitted (05-FEB-2002) Genome Sequencing Center, Washington
Direct Submission
TITLE

AUTHORS

TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 104787)

AUTHORS

TITLE Direct Submission
JOURNAL Submitted (09-MAR-2002)
Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Feb 20, 2002 this sequence version replaced g1:16543153.

----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 Summary Statistics
 Center project name: H_NH0495B16
 Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Pateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-563E24, 2000 bp overlap; the clone sequenced to the right is RP11-388N13. Actual start of this clone is at base position 13943 of RP11-563E24; actual end is at base position 104787 of RP11-495B16.

FEATURES The sequence of AC069095 has been incorporated into AC109638.

FEATURES

source
 1.104787
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2"
 /clone="RP11-495B16"
 /clone_id="RPCT-11"
 552..596
 /rpt_family="AT_rich"
 repeat_region
 2637..3165
 /rpt_family="L2"
 repeat_region
 3182..3356
 /rpt_family="L2"
 repeat_region
 3818..3893
 /rpt_family="MER2_type"
 repeat_region
 4009..4191
 /rpt_family="MER2_type"
 repeat_region
 4666..5182
 /rpt_family="L2"
 repeat_region
 5799..5818
 /rpt_family="(A)n"
 repeat_region
 6192..6528
 /rpt_family="MER2_type"
 repeat_region
 6700..6769
 /rpt_family="MERL_type"

repeat_region 6786..6959
 /rpt_family="MERL_type"
 repeat_region 6973..7025
 /rpt_family="(TC)n"
 repeat_region 7025..7057
 /rpt_family="(CA)n"
 repeat_region 7319..7785
 /rpt_family="ERV1"
 repeat_region 9500..10052
 /rpt_family="ERV1"
 repeat_region 10697..10820
 /rpt_family="MALR"
 repeat_region 10821..11231
 /rpt_family="MALR"
 repeat_region 11232..11468
 /rpt_family="MALR"
 repeat_region 11703..11724
 /rpt_family="AT_rich"
 repeat_region 12494..12548
 /rpt_family="MER2_type"
 repeat_region 12549..12940
 /rpt_family="MALR"
 repeat_region 12941..13189
 /rpt_family="MER2_type"
 repeat_region 13185..13261
 /rpt_family="MER2_type"
 repeat_region 14239..14260
 /rpt_family="AT_rich"
 repeat_region 14475..15193
 /rpt_family="L1"
 repeat_region 15747..15887
 /rpt_family="L1"
 repeat_region 15967..15992
 /rpt_family="AT_rich"
 repeat_region 16107..16127
 /rpt_family="AT_rich"
 repeat_region 16180..16303
 /rpt_family="MERL_type"
 repeat_region 16304..16612
 /rpt_family="MERL_type"
 repeat_region 16653..16825
 /rpt_family="L1"
 repeat_region 16858..17337
 /rpt_family="L1"
 repeat_region 17354..18118
 /rpt_family="L1"
 repeat_region 18119..18142
 /rpt_family="(TTG)n"
 repeat_region 18143..18402
 /rpt_family="Alu"
 repeat_region 18403..18849
 /rpt_family="L1"
 repeat_region 18853..18956
 /rpt_family="L1"
 repeat_region 18957..19008
 /rpt_family="MALR"
 repeat_region 19011..19414
 /rpt_family="L1"
 repeat_region 19419..19458
 /rpt_family="CT_rich"
 repeat_region 19558..19858
 /rpt_family="Alu"
 repeat_region 19900..19920
 /rpt_family="AT_rich"
 repeat_region 19946..19973
 /rpt_family="AT_rich"
 repeat_region 21137..21158
 /rpt_family="AT_rich"
 repeat_region 21636..21721
 /rpt_family="CT_rich"
 repeat_region 23013..23036
 /rpt_family="AT_rich"
 repeat_region 24267..24310

QY	2	CCAAATATGGCGGACGCATGTGTGGATGTGGATACCCCGAGGGGCGCAACAAAGCGCGGGGCA	61	
Db	78604	CCAAATATGGTGGCAGTGTATGTCAAGAGGGGTACCGTCTAGCAGCACCTTATGACACTGTGGGCA	78663	
QY	62	AGAGAGCGCTTTGAAGTGAATAAGTGAATGCAAGTGAACCGCTCTGGGCTGGGATATTGTGG	121	
Db	78664	AGAGAGCGCTTTAAAGTGAATAAGTGAATGCAAGTGAACCGCTCTGGGCTGGGATATTGTGC	78722	
QY	122	TTGTAATCTGTGGCATCTGCAAGAACCCATTATGGATC--TTTGCAATAGAAATGTCAAG	178	
Db	78723	TTGTAATCTGTGGCATCTGCAAGAACCCATTATGGATCCTTTTGGCAATAGAAATGTCAAG	78782	
QY	179	CTAACAGGCGCTCGCGCTACTTCAGAGAAGTGTACTGTGCATGGGGAGCTCTAACCATG	238	
Db	78783	CTAACAGGCTGTGCTGTACTTCTGAAAGATATACATCTTATGGGGCATGTCTAACCATTA	78842	
QY	239	CTTTTCACCTTCACCTGCATCTCTCGCTGGGCTCAAAACACAGACAGGTGTGTCCATTGGACA	298	
Db	78843	CTTTTCACCTTCACCTGCATCTCTCGCTGGGCTCAAAACACAGAGTATGTGTCCATTGGACA	78902	
QY	299	ACAGAGAGTGGGAATTTCCAAAAGTATGGGCACTAGAGAAAGACTTCTTCATCAAGCTTA	358	
Db	78903	ACAAAGAGTGGGAATTTCCAAAAGTATGGGCACTAGAGAAAGACTTCTTCATCAAGCTTA	78962	
QY	359	ATTGTTTGGTATTCATTAAATTGAATTCATTTCCCTGCTGTTACTTAATTACAAATTTGGATG	418	
Db	78963	ACTATTTGGTATTCATT - -AATGATTTTCCCTGCTGACCTAATTTAAATTTAGATG	79020	
QY	419	AACGTGTGTTTTTCTGCTTTGTTTTTTCAGTTTGCTGTTCTGTAGACCATATTTGATATTC	478	
Db	79021	AACGTGTGCTTTTCTGCTTTGTTTTTTCAGTTTGCTGTTCTGTAGACCATATTTATATTC	79079	
QY	479	TGTGTCAATTAAGTCAGCTGGATTCGG	508	
Db	79080	TGTGTCAATTAAGTCAGCTGGATTCG	79109	
RESULT 8	BC027396	1616 bp	linear	ROD 07-AUG-2007
LOCUS	BC027396	Mus musculus, ring-box 1, clone MGC:35907	IMAGE:4952242, mRNA,	
DEFINITION	BC027396	complete cds.		
ACCESSION	BC027396			
VERSION	BC027396.1	GI:20072075		
KEYWORDS	MGC.			
SOURCE	Mus musculus			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 1616)			

CTGCATCTCTCGATGGCTCAAAACCG

Db 242 TTCATTTCCACTGCATCTCGATGCGCTCAAACGAGCGAGGTGTGCCGTTGGACACA 301

Qy	302	GAGAGTGGGAATTC	CAAAAGATATGGG	CGACTAGGAAAAGACCTTCCGATCAAGCTTAAT	361
Db	302	GAGAGTGGGAGT	CCAGAAGTATGGCA	TTAGAAAAGACTTCCCGCAAGCGCTACCAT	361
Qy	362	GTTTGTGTAATTCAT	TAAATGACTTCCCGCTGTACCTAATTTCAAAATGGATGAAC	421	
Db	362	CTGTACTCGTCACTGA	-----CTTCCGTTAATTAATACATTTGATAGAACATG	412	
Qy	422	TGTGTTTTTCTCGT	TTGTTTTTTCACAGTTTGCTGTTCGTAGCCATATGTATTCTGT	481	
Db	413	GTCCCTTTTCTGTC	CTTTGTTTTTGAGAGTTGGTCTCCGAGCCATATGTATTGT	472	
Qy	482	GTCAATATTAAGTC	494		
Db	473	GTCAATATTAAGCC	485		

RESULT	9
AF142059	
LOCUS	AF142059
DEFINITION	327 bp mRNA linear PRI 14-JUL-1999
ACCESSION	AF142059
VERSION	AF142059.1 GI:4809215
KEYWORDS	Homo sapiens.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens.
REFERENCE	
COMMENTARY	
FEATURES	
ORIGIN	
BASES	
CDS	
ORF	
PROTEIN	
PEP	
BLAST	
FASTA	
GENBANK	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	
SWISSPROT	
PIR	
TrEMBL	
CD	
RefSeq	
NCBI	
GenBank	
EMBL	
DDBJ	

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 327)
Ohta,T., Michel,J.U., Schottelius,A.U. and Xiong,Y.
ROCI, a homolog of ApCII, represents a family of cullin partners
with an associated ubiquitin ligase activity
Mol. Cell 3 (4), 535-541 (1999)
99247022
2 (bases 1 to 327)
Ohta,T., Michel,J. and Xiong,Y.
Direct Submission
Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center,
University of North Carolina at Chapel Hill, Mason Farm Rd. and
Manning Dr., Chapel Hill, NC 27599-7295, USA
Location/Qualifiers

source	gene	CDS
1. .32/ /organism="Homo sapiens" /db_xref="taxon:9606"	1. .327 /gene="ROCl"	1. .327

BASE COUNT	ORIGIN
85 a	75 c 94 g 73 t

Query Match	64.4%	Score 327	DB 9	length 327
Best Local Similarity	100.0%	Pred. No. 3e-77		
Matches 327	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	7	ATGGCGGACGAGGATGTGATATACCCCGAGCGGCACCAACAGCGCGGCGCAAG	66	
Db	1	ATGGCGGACGAGGATGTGATATACCCCGAGCGGCACCAACAGCGCGGCGCAAG	60	
Qy	67	CGCTTTGAAGTGAANAAGTGAATGACATAGCCCTCTGGGCTGGGATATTGGTTGAT	126	
Db	61	CGCTTTGAAGTGAANAAGTGAATGACATAGCCCTCTGGGCTGGGATATTGGTTGAT	120	

OY	127	AACATGGCAATCGAGGAACAACATTATGATCTTTGCATAGAAATGCAGGTAAACCAG	186
Db	121	AACATGGCAATCGAGGAACAACACTTATGGATCTTTGCATAGAAATGCAGGTAAACCAG	180
OY	187	GCGTCGGCTACTTCAGAAGATGTAAGTCGATGCGATGGGAGTCTGTAAACCATGCTTTTCCAC	246
Db	181	GCGTCGGCTACTTCAGAAGATGTAAGTCGATGCGATGGGAGTCTGTAAACCATGCTTTTCCAC	240
OY	247	TTTCACATCCTCTCTCGCTGGGCTCAAACACAGACAGGTGTGTCCATTGGACAACAGAGAG	306
Db	241	TTTCACATCCTCTCTCGCTGGGCTCAAACACAGACAGGTGTGTCCATTGGACAACAGAGAG	300
OY	307	TGGGAATTCCAAAGATATGGGCACATAG	333
Db	301	TGGGAATTCCAAAGATATGGGCACATAG	327

RESULT 10
AF140599 LOCUS 504 bp mRNA linear ROD 11-MAY-1999
DEFINITION Mus musculus ring-box protein 1 (Rbx1) mRNA, complete cds.
ACCESSION AF140599
VERSION AF140599.1 GI:4769005
KEYWORDS
SOURCE Mus musculus.

REFERENCE	Eukaryota: Metazoa: Chordata: Craniala: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
AUTHORS	1 (bases 1 to 504) Kamur,T., Koepf,D.M., Conrad,M.N., Skowrya,D., Moreland,R.J., Iliopoulos,O., Lane,W.S., Kaelling,W.G., Jr., Ellledge,S.J., Conaway,R.C., Harper,J.W. and Conaway,J.W.
TITLE	Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase
JOURNAL	Science 284 (5414), 657-661 (1999)
MEDLINE	99234320
PUBMED	10213691
REFERENCE	2 (bases 1 to 504)
AUTHORS	Kamur,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.
TITLE	Direct Submission
JOURNAL	Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHWI, Oklahoma Med. Res. Fdn., 825 NE 13th St., Oklahoma City, OK 73104, USA

```

FEATURES
  source      location/Qualifiers
1. 504       /organism="Mus musculus"
           /db_xref="taxon:10090"
gene
1. 504
           /gene="Rbx1"

```

CDS	BASE COUNT
18..344 /gene="Rbx1" /note="component of VHL tumor suppressor complex and SCF ubiquitin ligase" /codon_start=1 /product="ring-box protein 1" /protein_id="Aad29716.1" /db_xref="GI:4769006" /translation="MAAAVDVDPGTSNAGKKRFEVKKMNAVALMAWDIVDNCAL CRNHIMDLCEQANQASATSECTVAMGVCHNAHFHHCISRLKTRQVCPIDNREME FQKIGH"	117 a 137 g 143 t 107 c

Query Match	Best Local Similarity	Score 323:	DB 10:	Length 504:
Matches 394: Conservative	0:	Mismatches 85:	Indels 10:	Gaps 1:
QY	2	CCAAATGCGCGCAGCGATGATGTGATACCCGAGCGCGCACACAGCGCGCGGCA	61	
Db	13	CCAAATGCGCGCGCGCGATGTGATGTGATACCCGAGCGCGCACACAGCGCGCGGCA	72	
QY	62	AGAGCGCGTTTGAAAGTGAAGAAAAGTGAATGAGATGAGCCCTTGCGGCTTGGGATATTGTGG	121	
Db	73	AGAGCGCGTTTGAAAGTGAAGAAAAGTGAATGAGATGAGCGCCCTTGCGGCTTGGGATATTGTGG	132	

Matches	42s; Conservative	0; Mismatches	64; Indels	22; Gaps	6b
QY	2	CCAAATATGGCGCAGCGATGATGTGATACCCGAGCGGACCAACAGCGCGGGCA	61		
Db	140577	CCAAATATGGCGAGTGCGCATGATGTGGATATACCCCAAGAGTAACAGC-----	140626		
QY	62	AGAAAGCGTTTGAAGTGAAGAAAGTGAATGTCAG-----TAGCCCTGTGGGCGGATATT	117		
Db	140627	---AGTCTTTGAAGTAAAAAAGTGAATGCAATGACGTACGCCCTTGGGCTTGGGATGTT	140683		
QY	118	GTGGTGTATTAACGTGTGCCATCTGCAGAGAACCAACCATTAATGATCTTTGCATAGATGTCAA	177		
Db	140684	GTGGTATATACGTGTGCCATCTGCAGAGATACACAGCATAGATC--TGATATGAATGTCAA	140741		
QY	178	GCTAACACAGCGCGTCGCTACTTTCAGAGAGATGTACTGTGCGATGGGAGTCTGTAAACAT	237		
Db	140742	GCTAACCAAGATGTGTGCACATTCAGAAAGTGTATGCTTGGACGGGGAGCCGTATAACCT	140801		
QY	238	GCTTTTCACTTCACATCGATCTCTGCGTGGCCCAAAACACGACAGTGTGTCCATTTGAC	297		
Db	140802	GCTTTTCACTT-CACGTCTCTCTCACGGCTCAAAACACACACAGCTGTGCTGTGGAC	140860		
QY	298	AACAGAGATGGGAAATTCCAAAGATGGAGGACATGTGAAGAAAGACTTCTCCATCAAGCTT	357		
Db	140861	AACAGACATATGGAATTCGCCAAGATGTGACACACGAAAAGAAATTTCTTCATCAAGCTT	140920		
QY	358	AATTGTTTTGTTATTCATTTAATGTGACTTTCCTGCTGTACCTAATTAACAAATTGGATG	417		
Db	140921	AACGTGTTTTGATTCATTTAA--TGACTTGCCCTCTGTCACTTAATATATATAGATGA	140979		
QY	418	GAATCTGTGTTTTTTTCGTCTTGTGTTTTTCAGATTGCTGTCTGTAGCCATATTTGATAT	477		
Db	140980	GAATCTGTG-TCTTTTCTGCTTGTCTTTGCCATTGTGCTGTCTGTCCAGCACATTGTATT	141038		
QY	478	CTGTGTCAAATAAAGTCCAGTTGGATTTCTGG	508		
Db	141039	CTGTGTCAAATAAAGTCCAGTTGGATTTCTAG	141069		
RESULT 12					
AC012636					
LOCUS	AC012636	175561 bp	DNA	linear	PRI 19-JUL-2001
DEFINITION					Homo sapiens chromosome 5 clone CTD-2201118, complete sequence.
ACCESSION	AC012636				
VERSION	AC012636.5	GI:14916146			
KEYWORDS	HTG.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE					
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 175561)				
JOURNAL	DOE Joint Genome Institute and Stanford Human Genome Center.				
AUTHORS	Direct Submission				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 175561)				
AUTHORS	DOE Joint Genome Institute.				
TITLE	Direct Submission				
JOURNAL	Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA				
REFERENCE	3 (bases 1 to 175561)				
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA				
COMMENT	On Jul 19, 2001 this sequence version replaced gi:13677006.				
	Draft Sequence Produced by DOE Joint Genome Institute				
	www.jgi.doe.gov				
	Finishing Completed at Stanford Human Genome Center				
	www.sngc.stanford.edu				
	Quality: Phrap Quality >=40 99.6% of sequence;				
	Estimated Total Number of Errors is 0.5.				
	STS Content:				
	SHGC-57819 G37430				

AUTHORS	ALLIET,P.M., SEDDIQI,N., BELKADI,L., LECOEUR,L. and PERIN,J.P.
TITLE	Direct Submission
JOURNAL	Submitted (23-APR-2002) U488, INSERM, 80, rue du General Leclerc, Le Kremlin-Bicetre 94270, France
FEATURES	Location/Qualifiers
source	1. .306 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="zyp3" /sex="male" /tissue_type="whole brain" /dev_stage="26-week fetus" /note="Caucasian" 1. .290 /note="similar to RBX1/ROCI/HRP1" /product="zyp protein" /protein_id="AAW21718.1" /db_xref="GI:20502055" /translation="NSGASKRRFEVKKRMNAVALMAMDIVDNCAICRNHIMDLICIQ ANQASATSEECTVAMGVCHNHFHCISRMILKTRQVCPLDNRWEVFGYGH"
BASE COUNT	84 a 70 c 80 g 72 t
ORIGIN	
Query Match	59.9%; Score 304.4; DB 9; Length 306;
Best Local Similarity	99.7%; Pred. No. 3,6e-71;
Matches 305; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	44 CCACAGGGGGGGGGGCAAGAAAGCCCTTGAAGTAAAGTGAATGCATGACGACCCCTCT 103
Db	1 CCACAGGGGGGGGGGCAAGAAAGCCCTTGAAGTAAAGTGAATGCATGACGACCCCTCT 60
OY	104 GGGCGCTGGATATTTGGTGTGATTAACCTGTCATCTGCAGAACCCATTAATGATCTTT 163
Db	61 GGGCGCTGGATATTTGGTGTGATTAACCTGTCATCTGCAGAACCCATTAATGATCTTT 120
OY	164 GCATGAATGTTCACCTTAACCAAGGGGTCCGTACTTCAAGAAAGTGTACTGTGCATGGG 223
Db	121 GCATGAATGTTCACCTTAACCAAGGGGTCCGTACTTCAAGAAAGTGTACTGTGCATGGG 180
OY	224 GAGTGTGAACCATCTTTTCACTTCCATCTGCATCTCGGTGCTCAAAACACGACAGG 283
Db	181 GAGTGTGAACCATCTTTTCACTTCCATCTGCATCTCGGTGCTCAAAACACGACAGG 240
OY	284 TGTGTCCATTGGACACAGAGAGTGGGATTTCCAAAGTATGGGCATGAGAAAAAGCTT 343
Db	241 TGTGTCCATTGGACACAGAGAGTGGGATTTCCAAAGTATGGGCATGAGAAAAAGCTT 300
OY	344 CTTCGA 349
Db	301 CTTCGA 306
RESULT 14	
LOCUS	AX281690 5347 bp DNA linear PAT 02-NOV-2001
DEFINITION	Sequence 99 from Patent WO0177389.
ACCESSION	AX281690
VERSION	AX281690.1 GI:16608941
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
AUTHORS	1 Shiffman,D., Somogyi,R., Lawn,R., Seilhammer,J.J., Porter,G.J., Mikita,T. and Tai,J.
TITLE	Genes expressed in foam cell differentiation
JOURNAL	Patent: WO 0177389-A 99 18-OCT-2001;
FEATURES	Incyte Genomics, Inc. (US) Location/Qualifiers
source	1. .5347 /organism="Homo sapiens"

